interferon beta or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as additional N-termini, or C-termini. For example, the conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast alpha -factor leader). Interferon beta receptor proteins can comprise peptides added to facilitate purification or identification of interferon beta (e.g., histidine/interferon-beta-la fusions). The amino acid sequence of interferon beta can also be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys (DYKDDDDK; SEQ ID NO: 61) (Hopp et al., Bio/Technology 6:1204,1988.) The latter sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. This sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing.

a2 cont

Please replace the paragraph beginning on page 34, line 5 with the following:

The full set of alanine substitution mutations are depicted in Table 1(next page). The names of the mutants specify the structural regions (helices (A (A1 (SEQ ID NO:45), A2 (SEQ ID NO:46)), B (B1 (SEQ ID NO:50), B2 (SEQ ID NO:51), C (C1 (SEQ ID NO:52), C2 (SEQ ID NO:53)), D (SEQ ID NO:56), E (SEQ ID NO:59)) and loops (AB1 (SEQ ID NO:47), AB2 (SEQ ID NO:48), AB3 (SEQ ID NO:49), CD1 (SEQ ID NO:54), CD2 (SEQ ID NO:55), DE1 (SEQ ID NO:57), DE2 (SEQ ID NO:58))) in which the mutations were introduced. The entire panel of alanine (serine) substitutions results in mutation of 65 of the 166 amino acids of human IFN-beta (SEQ ID NO: 60).

a3

Please replace the pending sequence listing with the enclosed sequence listing.

In the claims:

Please cancel claims 19-22 and 26-27 without prejudice or disclaimer as drawn to a non-elected invention. Please cancel claims 1-18, 23-25 and 28-31 and add new claims 32-43 as follows:

32. A polypeptide comprising

a4

the amino acid sequence of SEQ ID NO:60; and

a hinge, CH2 and CH3 domain of an immunoglobulin.

33. The polypeptide of claim 32, wherein the polypeptide is glycosylated at an amino acid in the amino acid sequence.

34. The polypeptide of claim 32, wherein the immunoglobulin is of the IgG class.

35. The polypeptide of claim 32, wherein the polypeptide further comprises a derivative.

36. The polypeptide of claim 35, wherein the derivative comprises a polyalkylglycol polymer.

37. The polypeptide of claim 36, wherein the polyalkylglycol polymer is coupled to the N-terminus of the amino acid sequence.

38. A polypeptide comprising

an amino acid sequence selected from the group consisting of SEQ ID NOs:45-59; and

a hinge, CH2 and CH3 domain of an immunoglobulin.

a4 Cont

39. The polypeptide of claim 38, wherein the polypeptide is glycosylated at an amino acid in the amino acid sequence.

40. The polypeptide of claim 38, wherein the immunoglobulin is of the IgG class.

41. The polypeptide of claim 38, wherein the polypeptide further comprises a derivative.

42. The polypeptide of claim 41, wherein the derivative comprises a polyalkylglycol polymer.

a^4

43. The polypeptide of claim 42, wherein the polyalkylglycol polymer is coupled to the N-terminus of the amino acid sequence.